Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) An isolated *rpoB* gene or gene fragment of a bacterium of the genus *Streptococcus* or the related genus *Enterococcus*, comprising a nucleic acid sequence selected from the group consisting of:

a. SEQ ID NOs: 8–10, 13, 15, 16, 20, 24, 29, and 30; and

b. the full-length complementary sequences of the nucleic acid sequences of (a)~~; and~~

~~c. sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b)~~.

2. (Currently Amended) An isolated *rpoB* gene of claim 1 wherein the bacterium is of the bacteria *Streptococcus anginosus*, comprising a nucleic acid sequence selected from the group consisting of:

a. SEQ ID NO:1 wherein:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T, and

N nucleotide represents A, T, C, G or I; and

b. the full-length complementary sequences of the nucleic acid sequences of (a)~~; and~~

~~c. sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b)~~.

3–6. (Canceled)

7. (Currently Amended) A mixture of oligonucleotides, comprising:

an equimolar mixture of oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence ~~and is at least 12 nucleotides in length~~ and comprises at ~~least 8~~ least 15 consecutive nucleotides of the full-length sequence set forth in SEQ ID NO:6 or SEQ ID NO:7, or at ~~least 8~~ least 15 consecutive nucleotides of the full-length complementary sequences thereof, where:

N represents, for the equimolar mixture, inosine or N represents, for the equimolar mixture, equimolar amounts of A, T, C, and G,

R represents A or G,

M represents A or C, and

Y represents C or T.

8. (Previously Presented) A mixture of oligonucleotides according to claim 7, wherein the equimolar mixture of oligonucleotides comprises 32 different oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides comprises at least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:6, or at least 15 consecutive nucleotides of the full-length complementary sequence thereof, where:

R represents A or G,

Y represents C or T,

M represents A or C, and

N represents A, T, C or G.

9. (Previously Presented) A mixture of oligonucleotides according to claim 7, wherein the equimolar mixture of oligonucleotides comprises 8 different oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides comprises at least

15 consecutive nucleotides of the sequence set forth in SEQ ID NO:6, or at least 15 consecutive nucleotides of the full-length complementary sequence thereof, where:

R represents A or G,

Y represents C or T,

M represents A or C, and

N represents inosine.

10. (Previously Presented) A mixture of oligonucleotides according to claim 7, wherein the equimolar mixture of oligonucleotides comprises 16 different oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides comprises at least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:7, or at least 15 consecutive nucleotides of the full-length complementary sequence thereof, where:

R represents A or G, and

N represents A, T, C or G

11. (Previously Presented) A mixture of oligonucleotides according to claim 7, wherein the equimolar mixture of oligonucleotides comprises 4 different oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides comprises at least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:7, or at least 15 consecutive nucleotides of the full-length complementary sequence thereof, where:

R represents A or G, and

N represents inosine.

12. (Previously Presented) A mixture of oligonucleotides according to claim 7, wherein each oligonucleotide in the equimolar mixture of oligonucleotides consists of the sequence set forth in SEQ ID NO:6, SEQ ID NO:7, or the full-length complementary sequences thereof.

13–14. (Canceled)

15. (Withdrawn) A method for detecting the presence of a bacterium of genus *Streptococcus* or of 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, comprising:

1. contacting at least one genus probe comprising a mixture of oligonucleotides as in claim 7, with a sample containing or possibly containing nucleic acids of at least one said bacterium, and

2. determining the formation or non-formation of a hybridization complex between said genus probe and nucleic acids of the specimen, wherein the presence of said bacterium in the specimen is indicated by formation of a hybridization complex.

16. (Withdrawn-Currently Amended) A method for detecting the presence of a bacterium of genus *Streptococcus* or of 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, comprising:

1. contacting amplification primers comprising mixtures of oligonucleotides as in claim 7, with a sample containing or possibly containing nucleic acids of at least one said bacterium, wherein:

a 5' primer comprises an equimolar mixture of oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and ~~is at least 12 nucleotides in length and~~ comprises at ~~least 8~~ least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:6, or at ~~least 8~~ least 15 consecutive nucleotides of the full-length complementary sequence thereof, and

a 3' primer comprises an equimolar mixture of oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and ~~is at least 12 nucleotides in length and~~ comprises at ~~least 8~~ least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:7, or at ~~least 8~~ least 15 consecutive nucleotides of the full-length complementary sequence thereof; and

2. amplifying nucleic acids by enzymatic polymerization reaction to determine the presence or absence of an amplification product, wherein occurrence of an amplification product indicates the presence of said bacterium in the sample.

17. (Canceled)

18. (Withdrawn-Currently Amended) A method for detecting whether a given species of a bacterium of genus *Streptococcus* or related genera is present in a sample, said given species of a bacterium selected from the group of species consisting of:

Streptococcus mutans, *Streptococcus oralis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus suis*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus difficilis*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus equinus*, *Streptococcus intermedius*, *Streptococcus mitis*, *Streptococcus bovis*, *Streptococcus alactolyticus*, *Streptococcus gallolyticus*, *Streptococcus macedonicus*, *Streptococcus infantarius*, *Streptococcus hominis*, *Granulicatella adjacens*, *Abiotrophia defectiva*, *Enterococcus avium*, *Enterococcus casselliflavus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus sacharolyticus*, *Gemella haemolysans*, and *Gemella morbillorum*,

the method comprising:

a) sequencing an amplified *rpoB* gene fragment of a bacterium using nucleotide primers comprising said oligonucleotide mixtures as in claim 7, wherein:

a 5' primer comprises an equimolar mixture of oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and ~~is at least 12 nucleotides in length and~~ comprises at ~~least 8~~ least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:6, or at ~~least 8~~ least 15 consecutive nucleotides of the full-length complementary sequence thereof, and

a 3' primer comprises an equimolar mixture of oligonucleotides, wherein each oligonucleotide in the equimolar mixture of oligonucleotides has a different sequence and ~~is at least 12 nucleotides in length and~~ comprises at ~~least 8~~ least 15 consecutive nucleotides of the sequence set forth in SEQ ID NO:7, or at ~~least 8~~ least 15 consecutive nucleotides of the full-length complementary sequence thereof; and

b) determining the presence or absence of the given species of said bacterium by comparing the sequence obtained of said fragment with the sequence of the complete *rpoB* gene of said bacterium or the sequence of a *rpoB* gene fragment of said bacterium respectively comprising said sequences selected from the group consisting of:

i) SEQ ID NOs:8-35; and

ii) the full-length complementary sequences of the nucleic acid sequences of (i); ~~and~~

~~iii) sequences having at least 98.7% homology to the nucleic acid sequences of (i) or (ii);~~

wherein the presence of said bacterium in the sample is determined if the obtained sequence of said fragment is identical to the known sequence of the *rpoB* gene or gene fragment of said bacterium.

19–21. (Canceled)

22. (Withdrawn-Currently Amended) The method according to claim 16, further comprising:

3. determining whether at least one species selected from the group consisting of *Streptococcus mutans*, *Streptococcus oralis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus suis*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus difficilis*, *Streptococcus dysgalactiae*,

Streptococcus equi, *Streptococcus equinus*, *Streptococcus intermedius*, *Streptococcus mitis*, *Streptococcus bovis*, *Streptococcus alactolyticus*, *Streptococcus gallolyticus*, *Streptococcus macedonicus*, *Streptococcus infantarius*, *Streptococcus hominis*, *Granulicatella adjacens*, *Abiotrophia defectiva*, *Enterococcus avium*, *Enterococcus casselliflavus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus sacharolyticus*, *Gemella haemolysans*, and *Gemella morbillorum*, is present in the sample by contacting the amplification product with at least one species probe comprising a nucleic acid sequence selected from the group consisting of:

(a) the sequences set forth in SEQ ID NOs:8-35; and

(b) the full-length complementary sequences of the nucleic acid sequences of (a); and

~~(c) sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b); and~~

4. determining formation or non-formation of a hybridization complex between said species probe and the amplification product, wherein the formation of a hybridization complex indicates the presence of said at least one species in the sample.

23. (Currently Amended) A set of isolated *rpoB* gene or gene fragments ~~oligonucleotides~~ comprising different *rpoB* gene or gene fragments ~~oligonucleotides~~ respectively comprising:

(a) the full-length sequences set forth in SEQ ID NOs:8–35; or

(b) the full-length complementary sequences of the sequences of (a); ~~or~~

~~(c) the sequences having at least 99.3% homology to the sequences of (a) or (b)~~.

24. (Currently Amended) A set of isolated *rpoB* gene or gene fragments ~~oligonucleotides~~ comprising different *rpoB* gene or gene fragments ~~oligonucleotides~~ respectively comprising:

(a) the full-length sequences set forth in SEQ ID NOs:8–35; and

(b) the full-length complementary sequences of the sequences of (a)~~; and~~

~~(c) sequences having at least 99.3% homology to the sequences of (a) and (b)~~.